

03CO 10-25-96  
RAW SEQUENCE LISTING  
PATENT APPLICATION US/08/704,159

TEAM 5 #3

DATE: 10/28/96  
TIME: 17:40:00

INPUT SET: S13439.raw

This Raw Listing contains the General  
Information Section and up to the first 5 pages.

## SEQUENCE LISTING

ENTERED

## (1) General Information:

(i) APPLICANT: Williams, James A.  
Thalley, Bruce S.(ii) TITLE OF INVENTION: Multivalent Vaccine For clostridium  
Botulinum Neurotoxin

(iii) NUMBER OF SEQUENCES: 82

## (iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Medlen & Carroll  
(B) STREET: 220 Montgomery Street, Suite 2200  
(C) CITY: San Francisco  
(D) STATE: California  
(E) COUNTRY: United States of America  
(F) ZIP: 94104

## (v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

## (vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US  
(B) FILING DATE:  
(C) CLASSIFICATION:

## (viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Ingolia, Diane E.  
(B) REGISTRATION NUMBER: 40,027  
(C) REFERENCE/DOCKET NUMBER: OPHD-02304

## (ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (415) 705-8410  
(B) TELEFAX: (415) 397-8338

## (2) INFORMATION FOR SEQ ID NO:1:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 base pairs  
(B) TYPE: nucleic acid

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47 (C) STRANDEDNESS: single  
48 (D) TOPOLOGY: linear  
49  
50 (ii) MOLECULE TYPE: DNA (genomic)  
51  
52

53 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:  
54  
55 GGAAATTTAG CTGCAGCATC TGAC  
56

24

57 (2) INFORMATION FOR SEQ ID NO:2:  
58  
59 (i) SEQUENCE CHARACTERISTICS:  
60 (A) LENGTH: 24 base pairs  
61 (B) TYPE: nucleic acid  
62 (C) STRANDEDNESS: single  
63 (D) TOPOLOGY: linear  
64  
65 (ii) MOLECULE TYPE: DNA (genomic)  
66  
67  
68

69 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:  
70  
71 TCTAGCAAAT TCGCTTGTGT TGAA  
72

24

73 (2) INFORMATION FOR SEQ ID NO:3:  
74  
75 (i) SEQUENCE CHARACTERISTICS:  
76 (A) LENGTH: 20 base pairs  
77 (B) TYPE: nucleic acid  
78 (C) STRANDEDNESS: single  
79 (D) TOPOLOGY: linear  
80  
81 (ii) MOLECULE TYPE: DNA (genomic)  
82  
83  
84

85 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:  
86  
87 CTCGCATATA GCATTAGACC  
88

20

89 (2) INFORMATION FOR SEQ ID NO:4:  
90  
91 (i) SEQUENCE CHARACTERISTICS:  
92 (A) LENGTH: 19 base pairs  
93 (B) TYPE: nucleic acid  
94 (C) STRANDEDNESS: single  
95 (D) TOPOLOGY: linear  
96  
97 (ii) MOLECULE TYPE: DNA (genomic)  
98  
99

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100
101
102 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:
103
104 CTATCTAGGC CTAAAGTAT
105
106 (2) INFORMATION FOR SEQ ID NO:5:
107
108 (i) SEQUENCE CHARACTERISTICS:
109 (A) LENGTH: 8133 base pairs
110 (B) TYPE: nucleic acid
111 (C) STRANDEDNESS: single
112 (D) TOPOLOGY: linear
113
114 (ii) MOLECULE TYPE: DNA (genomic)
115
116
117 (ix) FEATURE:
118 (A) NAME/KEY: CDS
119 (B) LOCATION: 1..8130
120
121
122 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:
123
124 ATG TCT TTA ATA TCT AAA GAA GAG TTA ATA AAA CTC GCA TAT AGC ATT 48
125 Met Ser Leu Ile Ser Lys Glu Glu Leu Ile Lys Leu Ala Tyr Ser Ile 15
126 1 5 10 15
127
128 AGA CCA AGA GAA AAT GAG TAT AAA ACT ATA CTA ACT AAT TTA GAC GAA 96
129 Arg Pro Arg Glu Asn Glu Tyr Lys Thr Ile Leu Thr Asn Leu Asp Glu 30
130 20 25
131
132 TAT AAT AAG TTA ACT ACA AAC AAT AAT GAA AAT AAA TAT TTG CAA TTA 144
133 Tyr Asn Lys Leu Thr Thr Asn Asn Asn Glu Asn Lys Tyr Leu Gln Leu 45
134 35 40
135
136 AAA AAA CTA AAT GAA TCA ATT GAT GTT TTT ATG AAT AAA TAT AAA ACT 192
137 Lys Lys Leu Asn Glu Ser Ile Asp Val Phe Met Asn Lys Tyr Lys Thr 60
138 50 55 60
139
140 TCA AGC AGA AAT AGA GCA CTC TCT AAT CTA AAA AAA GAT ATA TTA AAA 240
141 Ser Ser Arg Asn Arg Ala Leu Ser Asn Leu Lys Lys Asp Ile Leu Lys 80
142 65 70 75
143
144 GAA GTA ATT CTT ATT AAA AAT TCC AAT ACA AGC CCT GTA GAA AAA AAT 288
145 Glu Val Ile Leu Ile Lys Asn Ser Asn Thr Ser Pro Val Glu Lys Asn 95
146 85 90
147
148 TTA CAT TTT GTA TGG ATA GGT GGA GAA GTC AGT GAT ATT GCT CTT GAA 336
149 Leu His Phe Val Trp Ile Gly Gly Glu Val Ser Asp Ile Ala Leu Glu 110
150 100 105
151
152 TAC ATA AAA CAA TGG GCT GAT ATT AAT GCA GAA TAT AAT ATT AAA CTC 384

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# RAW SEQUENCE LISTING PATENT APPLICATION US/08/704,159

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153	Tyr Ile Lys Gln Trp Ala Asp Ile Asn Ala Glu Tyr Asn Ile Lys Leu	
154	115	120
155		
156	TGG TAT GAT AGT GAA GCA TTC TTA GTA AAT ACA CTA AAA AAG GCT ATA	432
157	Trp Tyr Asp Ser Glu Ala Phe Leu Val Asn Thr Leu Lys Lys Ala Ile	
158	130	135
159		
160	GTT GAA TCT TCT ACC ACT GAA GCA TTA CAG CTA CTA GAG GAA GAG ATT	480
161	Val Glu Ser Ser Thr Thr Glu Ala Leu Gln Leu Leu Glu Glu Ile	
162	145	150
163		
164	CAA AAT CCT CAA TTT GAT AAT ATG AAA TTT TAC AAA AAA AGG ATG GAA	528
165	Gln Asn Pro Gln Phe Asp Asn Met Lys Phe Tyr Lys Lys Arg Met Glu	
166	165	170
167		
168	TTT ATA TAT GAT AGA CAA AAA AGG TTT ATA AAT TAT TAT AAA TCT CAA	576
169	Phe Ile Tyr Asp Arg Gln Lys Arg Phe Ile Asn Tyr Tyr Lys Ser Gln	
170	180	185
171		
172	ATC AAT AAA CCT ACA GTA CCT ACA ATA GAT GAT ATT ATA AAG TCT CAT	624
173	Ile Asn Lys Pro Thr Val Pro Thr Ile Asp Asp Ile Ile Lys Ser His	
174	195	200
175		
176	CTA GTA TCT GAA TAT AAT AGA GAT GAA ACT GTA TTA GAA TCA TAT AGA	672
177	Leu Val Ser Glu Tyr Asn Arg Asp Glu Thr Val Leu Glu Ser Tyr Arg	
178	210	215
179		
180	ACA AAT TCT TTG AGA AAA ATA AAT AGT AAT CAT GGG ATA GAT ATC AGG	720
181	Thr Asn Ser Leu Arg Lys Ile Asn Ser Asn His Gly Ile Asp Ile Arg	
182	225	230
183		
184	GCT AAT AGT TTG TTT ACA GAA CAA GAG TTA TTA AAT ATT TAT AGT CAG	768
185	Ala Asn Ser Leu Phe Thr Glu Gln Glu Leu Leu Asn Ile Tyr Ser Gln	
186	245	250
187		
188	GAG TTG TTA AAT CGT GGA AAT TTA GCT GCA GCA TCT GAC ATA GTA AGA	816
189	Glu Leu Leu Asn Arg Gly Asn Leu Ala Ala Ala Ser Asp Ile Val Arg	
190	260	265
191		
192	TTA TTA GCC CTA AAA AAT TTT GGC GGA GTA TAT TTA GAT GTT GAT ATG	864
193	Leu Leu Ala Leu Lys Asn Phe Gly Gly Val Tyr Leu Asp Val Asp Met	
194	275	280
195		
196	CTT CCA GGT ATT CAC TCT GAT TTA TTT AAA ACA ATA TCT AGA CCT AGC	912
197	Leu Pro Gly Ile His Ser Asp Leu Phe Lys Thr Ile Ser Arg Pro Ser	
198	290	295
199		
200	TCT ATT GGA CTA GAC CGT TGG GAA ATG ATA AAA TTA GAG GCT ATT ATG	960
201	Ser Ile Gly Leu Asp Arg Trp Glu Met Ile Lys Leu Glu Ala Ile Met	
202	305	310
203		
204	AAG TAT AAA AAA TAT ATA AAT AAT TAT ACA TCA GAA AAC TTT GAT AAA	1008
205	Lys Tyr Lys Lys Tyr Ile Asn Asn Tyr Thr Ser Glu Asn Phe Asp Lys	

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335

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